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=> d his

     (FILE 'HOME' ENTERED AT 11:37:12 ON 24 NOV 2004)

     FILE 'CAPLUS, USPATFULL, EUROPATFULL, MEDLINE, BIOSIS' ENTERED AT
     11:38:01 ON 24 NOV 2004
L1          7112 S YEAST AND PEPTIDE LIBRARY
L2          6480 S L1 AND 1993
L3            11 S L1 AND PY<1993
L4             9 DUP REM L3 (2 DUPLICATES REMOVED)

     FILE 'STNGUIDE' ENTERED AT 11:40:50 ON 24 NOV 2004

     FILE 'CAPLUS, USPATFULL, EUROPATFULL, MEDLINE, BIOSIS' ENTERED AT
     11:42:06 ON 24 NOV 2004

     FILE 'STNGUIDE' ENTERED AT 11:42:08 ON 24 NOV 2004
L5             0 S EXPRESSION LIBRARY IN YEAST

     FILE 'CAPLUS, USPATFULL, EUROPATFULL, MEDLINE, BIOSIS' ENTERED AT
     11:51:15 ON 24 NOV 2004
L6         13641 S EXPRESSION LIBRARY AND YEAST
L7         13641 S EXPRESSION (W)LIBRARY AND YEAST
L8          7112 S PEPTIDE LIBRARY AND YEAST
L9          4868 S L7 (L) L8
L10          344 S SIGNAL PEPTIDE IN YEAST
L11            4 S L9 AND L10
L12           38 S L8 AND PY <1995
L13           26 DUP REM L12 (12 DUPLICATES REMOVED)
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L13 ANSWER 1 OF 26 EUROPATFULL COPYRIGHT 2004 WILA on STN

PATENT APPLICATION - PATENTANMELDUNG - DEMANDE DE BREVET

AN 585939 EUROPATFULL ED 20000227 EW 199410 FS OS STA B
TIEN TNF ligands.
TIDE TNF-Ligander.
TIFR Ligands du TNF.
IN Wallach, David, 24, Borochov Street, Rehovot, IL;
Bigda, Jacek, UL. Witosa 19B/1B, 80-809 Gdansk, PL;
Beletsky, Igor, Inst. of Theoretical Experimental Biophysics, RAS,
Puschino 142292, RU;
Mett, Igor, 15, Shpinoza Street, Rehovot, IL
PA YEDA RESEARCH AND DEVELOPMENT CO., Ltd., Weizmann Institute of Science,
P.O. Box 95, Rehovot 76 110, IL
SO Wila-EPZ-1994-H10-T1a
DS R AT; R BE; R CH; R DE; R DK; R ES; R FR; R GB; R GR; R IE; R IT; R LI;
R LU; R MC; R NL; R PT; R SE
PIT EPA2 EUROPAEISCHE PATENTANMELDUNG
PI **EP 585939 A2 19940309**
OD 19940309
AI EP 1993-114141 19930903
PRAI IL 1992-103051 19920903
IL 1993-106271 19930708
IC ICM C12N015-13
ICS C12P021-08 C07K015-28 A61K039-395 C12N015-12
C12N015-62 A61K037-02

GRANTED PATENT - ERTEILTES PATENT - BREVET DELIVRE

AN 585939 EUROPATFULL UP 20020207 EW 200205 FS PS
TIEN TNF ligands.
TIDE TNF-Liganden.
TIFR Ligands du TNF.
IN Wallach, David, 24, Borochov Street,, Rehovot, IL;
Bigda, Jacek, UL. Witosa 19B/1B, 80-809 Gdansk, PL;
Beletsky, Igor, Inst. of Theoretical Experimental Biophysics, RAS,
Puschino 142292, RU;
Mett, Igor, 60, Levin Epstein Street, Rehovot, IL
PA YEDA RESEARCH AND DEVELOPMENT CO., Ltd., Weizmann Institute of Science,
P.O. Box 95, Rehovot 76 110, IL
SO Wila-EPS-2002-H05-T1
DS R AT; R BE; R CH; R DE; R DK; R ES; R FR; R GB; R GR; R IE; R IT; R LI;
R LU; R MC; R NL; R PT; R SE
PIT EPB1 EUROPAEISCHE PATENTSCHRIFT
PI **EP 585939 B1 20020130**
OD 19940309
AI EP 1993-114141 19930903
PRAI IL 1992-103051 19920903
IL 1993-106271 19930708
REP EP 398327 A EP 444560 A
REN JOURNAL OF BIOLOGICAL CHEMISTRY., vol.267, no.9, 25 March 1992,
BALTIMORE US pages 5747 - 5750 MARSTERS, S.A. ET AL.; 'Identification of
cysteine-rich domains of the type 1 tumor necrosis factor receptor
involved in ligand binding'
IC ICM C12N015-13
ICS C12P021-08 C07K016-28 C07K016-42 A61K039-395
C12N015-12 C12N015-62

=> d l13 1-13 ti py au abs

L13 ANSWER 1 OF 26 EUROPATFULL COPYRIGHT 2004 WILA on STN
TIEN TNF ligands.
TIEN TNF ligands.
IN Wallach, David, 24, Borochov Street, Rehovot, IL;
Bigda, Jacek, UL. Witosa 19B/1B, 80-809 Gdansk, PL;
Beletsky, Igor, Inst. of Theoretical Experimental Biophysics, RAS, Puschino 142292, RU;
Mett, Igor, 15, Shpinoza Street, Rehovot, IL
IN Wallach, David, 24, Borochov Street,, Rehovot, IL;
Bigda, Jacek, UL. Witosa 19B/1B, 80-809 Gdansk, PL;
Beletsky, Igor, Inst. of Theoretical Experimental Biophysics, RAS, Puschino 142292, RU;
Mett, Igor, 60, Levin Epstein Street, Rehovot, IL

L13 ANSWER 2 OF 26 USPATFULL on STN
TI Cyclic peptide catalysts modeled on enzyme active sites
IN Atassi, M. Zouhair, 11743 Cawdor Way, Houston, TX, United States 77024
AB PEPZYMES.TM., chemically synthesized cyclic peptides, modeled on the active sites of naturally-occurring enzymes represented by chymotrypsin, trypsin, lysozyme, ribonuclease, urokinase, tissue plasminogen activator and their analogs are disclosed. The conformational constraints imposed on the peptide residues cause the amino acids of the peptide to assume a three-dimensional spatial relationship relative to the substrate that is essentially equivalent to that of the corresponding active site amino acids of the natural enzyme in its catalytically active state. The new cyclic peptides catalyze the same reaction as the native enzyme being modeled, but have amino acid sequences that are substantially shorter than the naturally-occurring enzymes, and do not occur in the same linear relationship in the naturally-occurring enzymes. Methods of producing PEPZYMES.TM. are described.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L13 ANSWER 3 OF 26 USPATFULL on STN
TI Phagemids coexpressing a surface receptor and a surface heterologous protein
IN Light, II, James Paul, San Diego, CA, United States
Lerner, Richard A., La Jolla, CA, United States
AB A filamentous phage is described comprising a matrix that includes a heterologous polypeptide fused to a first filamentous phage coat protein membrane anchor and a heterodimeric receptor comprised of first and second receptor polypeptides, wherein one of the receptor polypeptides is fused to a second filamentous phage coat protein membrane anchor. Filamentous phage expressing anchored heterodimeric receptors and dimers of heterologous polypeptides where a first subunit of the dimer is fused to a coat protein membrane anchor and the second subunit of the dimer is soluble heteromeric receptor are also described.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L13 ANSWER 4 OF 26 USPATFULL on STN
TI Determination of peptide motifs on MHC molecules
IN Rammensee, Hans-Georg, Tubingen, Germany, Federal Republic of
Falk, Kirsten, Sommerville, MA, United States
Rotzschke, Olaf, Sommerville, MA, United States
Stevanovic , Stefan, Plankstadt, Germany, Federal Republic of
Jung, Gunther, Tubingen, Germany, Federal Republic of
AB The present invention concerns a method for the determination of allele-specific peptide motifs on molecules of the major histocompatibility complex (MHC) of classes I and II as well as the peptide motifs which are obtainable by the method according to the

invention. In addition the use of the peptide motifs according to the invention for the production of a diagnostic or therapeutic agent is disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L13 ANSWER 5 OF 26 USPATFULL on STN
TI Heterodimeric receptor libraries using phagemids
IN Barbas, Carlos, La Jolla, CA, United States
Kang, Angray, Carlsbad, CA, United States
Lerner, Richard A., La Jolla, CA, United States
AB Filamentous phage comprising a matrix of cpVIII proteins encapsulating a genome encoding first and second polypeptides of an antogenously assembling receptor, such as an antibody, and a receptor comprised of the first and second polypeptides surface-integrated into the matrix via a filamentous phage coat protein membrane anchor domain fused to at least one of the polypeptides.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L13 ANSWER 6 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
TI Method for selection of biologically active peptide sequences
PY 1994
1994
1994
1997
1996
1996
1998
IN Doyle, Michael V.
AB An improved method for determining binding compds. from a mixture of similar compds., particularly a phage **peptide library**, is provided that is important especially to the fields of mol. biol. and drug discovery. The method comprises contacting a mixture of candidate compds. with a target mol. (e.g., receptor or ligand) presented on ≥2 different substrates (e.g., mammalian cell, recombinant insect cell, recombinant **yeast**, and recombinant bacteria).

L13 ANSWER 7 OF 26 USPATFULL on STN
TI **Peptide library** and screening method
IN Schatz, Peter J., Mountain View, CA, United States
Stemmer, Willem P. C., Menlo Park, CA, United States
AB A random **peptide library** constructed by transforming host cells with a collection of recombinant vectors that encode a fusion protein comprised of a DNA binding protein and a random peptide and also contain a binding site for the DNA binding protein can be used to screen for novel ligands. The screening method results in the formation of a complex comprising the fusion protein bound to a receptor through the random peptide ligand and to the recombinant DNA vector through the DNA binding protein.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L13 ANSWER 8 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1
TI Characterization of monoclonal antibodies to human immunodeficiency virus type 2 envelope glycoproteins
PY **1994**
AU Traincard, Francois; Rey-Cuille, Marie-Anne; Huon, Isabelle; Dartevelle, Sylvie; Mazie, Jean-Claude; Benichou, Serge
AB Twelve murine monoclonal antibodies (MAbs) to human immunodeficiency virus type 2 (isolate ROD) envelope glycoproteins have been generated and characterized. Nine MAbs were specific to the external gp125 and three

reacted with the transmembrane gp36. A large majority of MAbs displayed a significant affinity for the native gp140 precursor and were shown to bind to viral antigens on the surface of fixed HIV-2-infected cells. In Western blot anal., the 12 MAbs showed varying profiles of cross-reactivity, but none of the MAbs cross-reacted with the HIV-1LAI envelope. Six MAbs reacted exclusively with the homologous HIV-2ROD isolate whereas only two MAbs displayed cross-reactivity with HIV-2ROD, HIV-2EHO, and SIV mac251. The four other MAbs cross-reacted with either HIV-2EHO or SIV mac251. Results of competitive binding assays indicated that the three anti-gp36 MAbs shared the same competition group, whereas at least eight competition groups were defined with the nine anti-gp125 MAbs. The epitopes of the three anti-gp36 and four anti-gp125 MAbs were delineated using synthetic peptides or by immunol. screening of an SIV mac251 **peptide library** expressed in **yeast**.
The anti-gp36 MAbs are directed against the same domain of the transmembrane gp36 corresponding to the major antigenic determinant of HIV-2 and HIV-1. The four anti-gp125 MAbs recognize four distinct epitopes localized in the V2, V3, and C1 domains. None of the 12 MAbs displayed neutralizing activity against HIV-2ROD, including the 2 MAbs directed against the V2 and V3 domains. These MAbs represent the largest collection of antibodies to envelope glycoproteins of HIV-2 reported to date and are available for a broad range of applications.

L13 ANSWER 9 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 2
TI Characterization and mapping of a B-cell immunogenic domain in hepatitis C virus E2 glycoprotein using a **yeast peptide library**
PY **1994**
AU Mink, Michael A.; Benichou, Serge; Madaule, Pascal; Tiollais, Pierre; Prince, Alfred M.; Inchauspe, Genevieve
AB To identify conserved humoral antigenic determinants within the hepatitis C virus (HCV) envelope protein E2, the authors expressed a **peptide library** containing random short fragments of the HCV envelope in **yeast**. Clones were identified using a monospecific rabbit antibody to a region downstream of the E2 hypervariable region. The clones define the limits of two original antigenic domains: a major one (aa 493-576) and a minor one (aa 535-606). The major antigenic domain maps in a region that displays a high degree of homol. within a (HCV) subtype (92-97.6% identity). **Yeast**-encoded determinants were characterized by Western blot anal., N-glycosidase F digestion, and using a panel of synthetic peptides. The data suggest that the major antigenic domain contains at least two determinants, one of them mimicked by an 18-mer peptide (aa 514-531). ELISA and competitive inhibition assays demonstrated that: (1) the determinants appear subtype 1a-specific, (2) seroprevalence of antibody to the determinants is rather low (20.6%), and (3) donors show a heterologous response to the different determinants. Antibody response to the E2 determinants was studied in HCV-infected chimpanzees and post-transfusion-associated NANB hepatitis cases. The antibody response was found during chronic infection and may not be effective for virus clearance.

L13 ANSWER 10 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
TI Construction of **peptide library** and its use in screening for receptor ligands
PY 1993
1993
1993
1994
2002
2002
IN Schatz, Peter J.; Cull, Millard G.; Miller, Jeff F.; Stemmer, Willem Peter Christian

AB A method of constructing a random **peptide library** comprises preparing a DNA vector containing a gene for a DNA binding protein and a binding site for that protein. The vector is modified by insertion of coding sequences for random peptides into the DNA binding protein gene such that fusion proteins are encoded. Host cells are transformed with these vectors and cultured to produce the fusion proteins. To screen the **peptide library**, the cells are lysed under conditions allowing the fusion protein to remain bound to the vector encoding the fusion protein, and the lysate is contacted with an (immobilized) receptor. This screening process can be repeated. Plasmid pMC5, containing 2 lacOs sequences and a lacI gene, was prepared and oligonucleotides encoding random dodecamers were inserted. These chimeric lacI genes were expressed in Escherichia coli and the fusion proteins in E. coli lysates were screened with anti-dynorphin antibody. Over 50 ligands were identified in this manner and their sequences were determined by plasmid sequencing.

L13 ANSWER 11 OF 26 USPATFULL on STN
TI **Peptide library** and screening method
IN Schatz, Peter J., Los Altos, CA, United States
Cull, Millard G., Oakland, CA, United States
Miller, Jeff F., Los Angeles, CA, United States
AB A random **peptide library** constructed by transforming host cells with a collection of recombinant vectors that encode a fusion protein comprised of a DNA binding protein and a random peptide and also encode a binding site for the DNA binding protein can be used to screen for novel ligands. The screening method results in the formation of a complex comprising the fusion protein bound to a receptor through the random peptide ligand and to the recombinant DNA vector through the DNA binding protein.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L13 ANSWER 12 OF 26 USPATFULL on STN
TI Virulence associated proteins in Borrelia burgdorferi (BB)
IN Norris, Steven J., Houston, TX, United States
Barbour, Alan G., San Antonio, TX, United States
AB The invention relates to a DNA segment encoding a Borrelia burgdorferi antigenic polypeptide. The invention also relates to a purified 30 kDa polypeptide isolated from a virulent strain of B. burgdorferi and to epitopic segments of the polypeptide with immunogenic potential. The 30 kDa protein provides a route for the development of immunodiagnostics for Lyme disease and related disorders. The 30 kDa protein and related amino acid and DNA sequences may also be used for the immunization, for the detection of B. burgdorferi in human or animal tissues or body fluids, and also for the generation of specific antibodies for use in diagnosis, epidemiology, and prevention of Lyme disease.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L13 ANSWER 13 OF 26 USPATFULL on STN
TI Directed evolution of novel binding proteins
IN Ladner, Robert C., Ijamsville, MD, United States
Guterman, Sonia K., Belmont, MA, United States
Roberts, Bruce L., Milford, MA, United States
Markland, William, Milford, MA, United States
Ley, Arthur C., Newton, MA, United States
Kent, Rachel B., Boxborough, MA, United States
AB In order to obtain a novel binding protein against a chosen target, DNA molecules, each encoding a protein comprising one of a family of similar potential binding domains and a structural signal calling for the display of the protein on the outer surface of a chosen bacterial cell,

bacterial spore or phage (genetic package) are introduced into a genetic package. The protein is expressed and the potential binding domain is displayed on the outer surface of the package. The cells or viruses bearing the binding domains which recognize the target molecule are isolated and amplified. The successful binding domains are then characterized. One or more of these successful binding domains is used as a model for the design of a new family of potential binding domains, and the process is repeated until a novel binding domain having a desired affinity for the target molecule is obtained. In one embodiment, the first family of potential binding domains is related to bovine pancreatic trypsin inhibitor, the genetic package is M13 phage, and the protein includes the outer surface transport signal of the M13 gene III protein.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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=> d his

     (FILE 'HOME' ENTERED AT 12:23:40 ON 24 NOV 2004)

     FILE 'MEDLINE' ENTERED AT 12:23:48 ON 24 NOV 2004
L1           363 S SIGNAL PEPTIDE AND YEAST
L2           141 S  PEPTIDE LIBRARY AND YEAST
L3             1 S L1 AND L2
L4             0 S PEPTIDE WITH TRANSPORT AND PERIPLASMIC NEAR YEAST
L5           119 S PROTEIN SECRETION AND YEAST
L6            35 S L5 AND PY <1993
L7             0 S SCREENING ASSAY AND L6
L8             0 S L6 AND PEPTIDE SECRETION
L9             3 S L6 AND PERIPLASMIC
```

L9 ANSWER 1 OF 3 MEDLINE on STN
AN 93049050 MEDLINE
DN PubMed ID: 1425485
TI Secretion of peptides and proteins lacking hydrophobic signal sequences: the role of adenosine triphosphate-driven membrane translocators.
AU Kuchler K; Thorner J
CS Department of Molecules Genetics, University and Biocenter Vienna, Austria.
NC GM-2184 (NIGMS)
SO Endocrine reviews, **(1992 Aug)** 13 (3) 499-514. Ref: 201
Journal code: 8006258. ISSN: 0163-769X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals
EM 199212
ED Entered STN: 19930122
Last Updated on STN: 19930122
Entered Medline: 19921217
AB In this review, we will emphasize the role of ATP-dependent membrane transporters in protein export and intracellular protein trafficking in prokaryotic and eukaryotic cells. ATP-binding-cassette (ABC)-transport proteins, also termed "traffic ATPases," belong to a superfamily of ubiquitous ATP-driven membrane transporters that share extensive sequence similarity and highly conserved domain organization. They are implicated in a remarkable variety of transmembrane transport processes, including the transport of ions, heavy metals, sugars, anticancer drugs, amino acids, oligopeptides, and proteins. Bacterial ABC-proteins include the well-characterized **periplasmic** permeases involved in nutrient uptake, but also include **protein secretion** systems, such as the exporter for the Escherichia coli enterotoxin hemolysin A. Prominent eukaryotic members of this superfamily include the human P-glycoprotein (which is associated with the phenomenon of multiple drug resistance in tumor cells), the product of the cystic fibrosis gene (CFTR), the gene (pfmdr) implicated in chloroquine resistance of the malarial parasite, putative peptide transporters encoded at the locus for the class II major histocompatibility complex (MHC), and the **yeast** Ste6 transporter which mediates export of a peptide hormone that lacks a classical hydrophobic signal peptide. The well-established function of prokaryotic ABC-transporters in the secretion of proteins without typical signal sequences, and the example set by the Ste6 transporter, have led to the reasonable hypothesis that certain ABC-proteins in animal cells may be operating by a similar mechanism to mediate the export of a new class of secretory proteins, those lacking a classical hydrophobic signal peptide.
CT Check Tags: Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
*Adenosine Triphosphate: PD, pharmacology
Amino Acid Sequence
Animals
Bacterial Proteins: SE, secretion
Carrier Proteins: CH, chemistry
*Carrier Proteins: PH, physiology
*Cell Membrane: ME, metabolism
Molecular Sequence Data
*Peptides: SE, secretion
*Protein Sorting Signals: SE, secretion
RN 56-65-5 (Adenosine Triphosphate); 61194-02-3 (mating factor)
CN 0 (Bacterial Proteins); 0 (Carrier Proteins); 0 (Peptides); 0 (Protein Sorting Signals)

L9 ANSWER 2 OF 3 MEDLINE on STN
AN 91151611 MEDLINE
DN PubMed ID: 1366833
TI Optimal chemostat cascades for **periplasmic** protein production.
AU Davis R H; Ramirez W F; Chatterjee A
CS Department of Chemical Engineering, University of Colorado, Boulder 80309-0424.
SO Biotechnology progress, **(1990 Nov-Dec)** 6 (6) 430-6.
Journal code: 8506292. ISSN: 8756-7938.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Biotechnology
EM 199104
ED Entered STN: 19950809
Last Updated on STN: 19970203
Entered Medline: 19910410
AB This theoretical work predicts the optimal system design for the steady-state production of secreted protein in a chemostat cascade, using bakers' **yeast** (Saccharomyces cerevisiae) as the host organism. The protein of interest, mutant invertase, is secreted to the **periplasmic** space instead of the culture medium on account of its large size. This work uses the secretion model developed and tested by Park and Ramirez (1988). It is shown that the highest productivity is achieved when the chemostat cascade contains two stages, although the improvement over the single-stage productivity is small. When no recycle is used, the advantage of two stages results from the tradeoff between maximizing the cell concentration and maximizing the rate of protein production per cell. When recycle is used, the cell concentration and protein productivity are increased, and the advantage of two stages results from the tradeoff between maximizing the specific protein production rate and maximizing the specific **protein secretion** rate. Cascades with three stages were also investigated, but these were found to have no improvement over the corresponding two-stage cascades.
CT Check Tags: Support, U.S. Gov't, Non-P.H.S.
Cloning, Molecular
Genetic Engineering
*Glycoside Hydrolases: BI, biosynthesis
Glycoside Hydrolases: GE, genetics
Glycoside Hydrolases: SE, secretion
Kinetics
Mutation
*Recombinant Proteins: BI, biosynthesis
*Saccharomyces cerevisiae: EN, enzymology
Saccharomyces cerevisiae: GD, growth & development
beta-Fructofuranosidase
CN 0 (Recombinant Proteins); EC 3.2.1. (Glycoside Hydrolases); EC 3.2.1.26 (beta-Fructofuranosidase)

L9 ANSWER 3 OF 3 MEDLINE on STN
AN 86195980 MEDLINE
DN PubMed ID: 3009432
TI **Protein secretion** from Saccharomyces cerevisiae directed by the prepro-alpha-factor leader region.
AU Zsebo K M; Lu H S; Fieschko J C; Goldstein L; Davis J; Duker K; Suggs S V; Lai P H; Bitter G A
SO Journal of biological chemistry, **(1986 May 5)** 261 (13) 5858-65.
Journal code: 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English

FS Priority Journals
EM 198605
ED Entered STN: 19900321
Last Updated on STN: 20030128
Entered Medline: 19860530
AB The Saccharomyces cerevisiae secretory process was studied by evaluating secretion efficiency, processing efficiency, and the efficiency of protein folding for hybrid proteins containing the **yeast** prepro-alpha-factor leader region. Secretion of three proteins, beta-endorphin, calcitonin, and a consensus alpha-interferon (IFN-Con1), were compared in terms of secretion efficiency into the culture medium, beta-Endorphin and calcitonin, both small proteins, were found to be efficiently secreted from logarithmically grown cells. In contrast, the larger IFN-Con1 accumulated in the **periplasmic** space and cell wall. The glycosylated, unprocessed prepro-alpha-factor/IFN-Con1 fusion protein was also found to be secreted into the culture medium. The presence of (Glu-Ala) dipeptides in the alpha-factor spacer peptide increased the efficiency of cleavage at Lys-Arg in the prepro-alpha-factor/IFN-Con1 protein fusion. Purified secreted IFN-Con1 was structurally characterized to determine the effect of passage through the **yeast** secretory pathway on the fidelity and efficiency of protein folding. The disulfide structure of the secreted protein was found to be identical with that reported for the native human alpha-interferons.
CT Amino Acid Sequence
Base Sequence
Cloning, Molecular
DNA Restriction Enzymes
Endorphins: GE, genetics
*Fungal Proteins: GE, genetics
*Genes, Fungal
*Genes, Structural
Genetic Vectors
Kinetics
Peptides: GE, genetics
Plasmids
Protein Hybridization
*Protein Precursors: GE, genetics
*Saccharomyces cerevisiae: GE, genetics
Saccharomyces cerevisiae: ME, metabolism
*Saccharomyces cerevisiae Proteins
Translation, Genetic
beta-Endorphin
RN 60617-12-1 (beta-Endorphin); 61194-02-3 (mating factor)
CN 0 (Endorphins); 0 (Fungal Proteins); 0 (Genetic Vectors); 0 (MF alpha protein, S cerevisiae); 0 (Peptides); 0 (Plasmids); 0 (Protein Precursors); 0 (Saccharomyces cerevisiae Proteins); EC 3.1.21 (DNA Restriction Enzymes)

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     FILE 'MEDLINE' ENTERED AT 12:23:48 ON 24 NOV 2004
L1          363 S SIGNAL PEPTIDE AND YEAST
L2          141 S  PEPTIDE LIBRARY AND YEAST
L3            1 S L1 AND L2
L4            0 S PEPTIDE WITH TRANSPORT AND PERIPLASMIC NEAR YEAST
L5          119 S PROTEIN SECRETION AND YEAST
L6           35 S L5 AND PY <1993
L7            0 S SCREENING ASSAY AND L6
L8            0 S L6 AND PEPTIDE SECRETION
L9            3 S L6 AND PERIPLASMIC
L10           0 S PEPTIDE EXPRESSION AND SIGNAL PEPTIDE AND YEAST
L11           1 S PEPTIDE WITH SIGNAL WITH SEQUENCE AND YEAST

     FILE 'STNGUIDE' ENTERED AT 12:32:59 ON 24 NOV 2004
L12           0 S PEPTIDE WITH LIBRARY AND YEAST
L13           0 S YEAST

     FILE 'MEDLINE' ENTERED AT 12:34:02 ON 24 NOV 2004
L14           3 S PEPTIDE WITH EXPRESSION AND YEAST
L15           9 S SIGNAL WITH PEPTIDE AND PROTEIN SECRETION AND YEAST
```

L15 ANSWER 1 OF 9 MEDLINE on STN
AN 2003268540 MEDLINE
DN PubMed ID: 12794930
TI Development of a reporter system for the **yeast** Schwanniomyces occidentalis: influence of DNA composition and codon usage.
AU Janatova Ivana; Costaglioli Patricia; Wesche Jorgen; Masson Jean-Michel; Meilhoc Eliane
CS Laboratory of Cell Reproduction, Institute of Microbiology, Academy of Sciences of the Czech Republic, Videnska 1083, 142 20 Prague 4, Czech Republic.. janatova@biomed.cas.cz
SO Yeast (Chichester, England), (2003 Jun) 20 (8) 687-701.
Journal code: 8607637. ISSN: 0749-503X.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200308
ED Entered STN: 20030610
Last Updated on STN: 20030823
Entered Medline: 20030822

L15 ANSWER 2 OF 9 MEDLINE on STN
AN 2000470746 MEDLINE
DN PubMed ID: 10974125
TI **Signal peptide**-dependent protein transport in Bacillus subtilis: a genome-based survey of the secretome.
AU Tjalsma H; Bolhuis A; Jongbloed J D; Bron S; van Dijl J M
CS Department of Genetics, Groningen Biomolecular Sciences and Biotechnology Institute, 9750 AA Haren, The Netherlands.
SO Microbiology and molecular biology reviews : MMBR, (2000 Sep) 64 (3) 515-47. Ref: 338
Journal code: 9706653. ISSN: 1092-2172.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals
EM 200010
ED Entered STN: 20001012
Last Updated on STN: 20001012
Entered Medline: 20001002

L15 ANSWER 3 OF 9 MEDLINE on STN
AN 97207238 MEDLINE
DN PubMed ID: 9054373
TI Expression, secretion, and processing of rice alpha-amylase in the **yeast** Yarrowia lipolytica.
AU Park C S; Chang C C; Kim J Y; Ogrydziak D M; Ryu D D
CS Biochemical Engineering Program, Department of Chemical Engineering and Material Science, University of California, Davis, California 95616, USA.
SO Journal of biological chemistry, (1997 Mar 14) 272 (11) 6876-81.
Journal code: 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199704
ED Entered STN: 19970424
Last Updated on STN: 19990129
Entered Medline: 19970417

L15 ANSWER 4 OF 9 MEDLINE on STN
AN 93049050 MEDLINE
DN PubMed ID: 1425485
TI Secretion of peptides and proteins lacking hydrophobic signal sequences: the role of adenosine triphosphate-driven membrane translocators.
AU Kuchler K; Thorner J
CS Department of Molecules Genetics, University and Biocenter Vienna, Austria.
NC GM-2184 (NIGMS)
SO Endocrine reviews, (1992 Aug) 13 (3) 499-514. Ref: 201
Journal code: 8006258. ISSN: 0163-769X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals
EM 199212
ED Entered STN: 19930122
Last Updated on STN: 19930122
Entered Medline: 19921217

L15 ANSWER 5 OF 9 MEDLINE on STN
AN 93004943 MEDLINE
DN PubMed ID: 1327299
TI Signal recognition particle receptor is important for cell growth and **protein secretion** in Saccharomyces cerevisiae.
AU Ogg S C; Poritz M A; Walter P
CS Department of Biochemistry and Biophysics, University of California, Medical School, San Francisco 94143-0448.
SO Molecular biology of the cell, (1992 Aug) 3 (8) 895-911.
Journal code: 9201390. ISSN: 1059-1524.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-M77274
EM 199211
ED Entered STN: 19930122
Last Updated on STN: 19930122
Entered Medline: 19921104

=> d l15 6-9

L15 ANSWER 6 OF 9 MEDLINE on STN
AN 90215305 MEDLINE
DN PubMed ID: 2182392
TI Changes in a mammalian signal sequence required for efficient **protein secretion** by **yeasts**.
AU Ngsee J K; Smith M
CS Department of Biological Sciences, Stanford University, CA 94305-5020.
SO Gene, (1990 Feb 14) 86 (2) 251-5.
Journal code: 7706761. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199005
ED Entered STN: 19900622
Last Updated on STN: 19900622

Entered Medline: 19900516

L15 ANSWER 7 OF 9 MEDLINE on STN
AN 89389494 MEDLINE
DN PubMed ID: 2675490
TI Secretion and glycosylation of Clostridium thermocellum endoglucanase A encoded by the celA gene in Saccharomyces cerevisiae.
AU Benitez J; Silva A; Vazquez R; Noa M D; Hollenberg C P
CS Departamento de Genetica, Centro Nacional de Investigaciones Cientificas, La Habana, Cuba.
SO Yeast (Chichester, England), (1989 Jul-Aug) 5 (4) 299-306.
Journal code: 8607637. ISSN: 0749-503X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198910
ED Entered STN: 19900309
Last Updated on STN: 19900309
Entered Medline: 19891020

L15 ANSWER 8 OF 9 MEDLINE on STN
AN 89284207 MEDLINE
DN PubMed ID: 2660366
TI Genetic dissection of the early stages of **protein secretion** in **yeast**.
AU Deshaies R J; Kepes F; Bohni P C
SO Trends in genetics : TIG, (1989 Mar) 5 (3) 87-93. Ref: 34
Journal code: 8507085. ISSN: 0168-9525.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 198907
ED Entered STN: 19900309
Last Updated on STN: 19900309
Entered Medline: 19890718

L15 ANSWER 9 OF 9 MEDLINE on STN
AN 88246048 MEDLINE
DN PubMed ID: 3288832
TI Defective Escherichia coli **signal peptides** function in **yeast**.
AU Pines O; Lunn C A; Inouye M
CS Department of Biochemistry, State University of New York, Stony Brook 11794.
NC GM10362 (NIGMS)
GM19043 (NIGMS)
SO Molecular microbiology, (1988 Mar) 2 (2) 209-17.
Journal code: 8712028. ISSN: 0950-382X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198807
ED Entered STN: 19900308
Last Updated on STN: 19970203
Entered Medline: 19880727